

UniProtKB/Swiss-Prot entry O84883

Entry information

Entry name	Y875_CHLTR
Primary accession number	O84883
Secondary accession numbers	None
Integrated into Swiss-Prot on	April 27, 2001
Sequence was last modified on	November 1, 1998 (Sequence version 1)
Annotations were last modified on	October 31, 2006 (Entry version 28)

Name and origin of the protein

Protein name	Protein CT_875
Synonyms	None
Gene name	OrderedLocusNames: CT_875
From	Chlamydia trachomatis [TaxID: 813] [HAMAP proteome]
Taxonomy	Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

References

[1] NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
STRAIN=D/UW-3/Cx;
DOI=10.1126/science.282.5389.754; PubMed=9784136
Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V., Davis R.W.;
"Genome sequence of an obligate intracellular pathogen of humans: Chlamydia trachomatis.";
Science 282:754-759(1998).

Comments

- **SIMILARITY:** To C.muridarum TC_0268.

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Cross-references

Sequence databases	
EMBL	AE001273; AAC68473.1; -; Genomic DNA.
PIR	C71460; C71460.
2D gel databases	
PHCI-2DPAGE	O84883; -.
Genome annotation databases	
GenomeReviews	AE001273 GR; CT_875.
KEGG	ctr:CT875; -.
Other	
Implicit links to	CMR; ProDom; HOGENOM; BLOCKS; ProtoNet; ModBase; UniRef.

Keywords

Complete proteome.

Features

Key	From	To	Length	Description	FTId
CHAIN	1	591	591	Protein CT_875. PRO_0000218349	

Sequence information

Length: 591 AA [This is the length of the unprocessed precursor]
Molecular weight: 66076 Da [This is the MW of the unprocessed precursor]
CRC64: B21C0127FDBB2EC8 [This is a checksum on the sequence]

102030405060

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MSIRGVGGNG NSRIPSHNGD GSNRRSQNTK GNNKVEDRVC SLYSSRSNEN RESPYAVVDV
70 80 90 100 110 120
SSMIESTPTS GETTRASRGV FSRFQRLVR VADKVRRAVQ CAWSSVSTRR SSATRAAESG
130 140 150 160 170 180
SSSRTARGAS SGYREYPSA ARGLRLMFTD FWRTRVLRQT SPMAGVFGNL DVNEARLMAA
190 200 210 220 230 240
YTSECADHLE ANKLAGPDGV AAAREIAKRW EQRVRDLQDK GAARKLLNDP LGRRTPNYQS
250 260 270 280 290 300
KNPGEYTVGN SMFYDGPQVA NLQNVDTGFV LDMSNLSDVV LSREIQTGLR ARATLEESMP
310 320 330 340 350 360
MLENLEERFR RLQETCDAAR TEIEESGWTR ESASRMEGDE AQGPSRAQQA FQSFVNECNS
370 380 390 400 410 420
IEFSFGSFG E HVRVLCARVS RGLAAAGEAI RRCFSCCKGS THRYAPRDDL SPEGASLAET
430 440 450 460 470 480
LARFADDMGI ERGADGTIDI PLVDDWRRGV PSIEGEGSDS IYEIMMPIYE VMDMDLETRR
490 500 510 520 530 540
SFAVQOGHYQ DPRASYDLP RASDYDLPRS PYPTPLPPR YQLQNMDVEA GFREAVYASF
550 560 570 580 590
VAGMNYVVT QPQERIPNSQ QVEGILRDML TNGSQTFRDL MRRWNREVDR E

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